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    $0.30 Estimated cost this search
    $0.30 Estimated total session cost   0.087 DialUnits

File 155:MEDLINE(R) 1966-2002/Jan W4

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Set   Items  Description
S1     1937  VLP OR VIRUS(W)LIKE(W)PARTIC?
S2      252  EMPTY(N)CAPSID?
S3     2185  S1 OR S2
S4    41021  HEPATITIS(W)B
S5      109  S3 AND S4
S6       64  ROTAVIRUS AND S3
S7        3  ALPHAVIRUS AND S3
S8        0  SINDBIS AND S3
S9       14  SEMLIKI AND S3
S10    2977  NONINFECTIOUS OR NON(W)INFECTIOUS
S11    1077  ALPHAVIR?
S12       3  S10 AND S11
S13     767  NORWALK
S14      52  S3 AND S13
S15    3508  FOOT(2W)MOUTH
S16      15  S15 AND S3
S17     220  RETROVIR? AND S3
S18      10  TOBACCO(W)MOSAIC AND S3
S19       3  FLOCK(W)HOUSE AND S3
S20   56899  ENCEPHAL?
S21      41  S20 AND S3
? t s9/7/3 6

 9/7/3
DIALOG(R)File 155:MEDLINE(R)
10436370  20057909  PMID: 10590104
 Rainbow trout sleeping disease virus is an atypical alphavirus.
 Villoing S; Bearzotti M; Chilmonczyk S; Castric J; Bremont M
 Unite de Virologie et Immunologie Moleculaires, Institut National de la
Recherche Agronomique, 78352 Jouy-en-Josas Cedex, France.
 Journal of virology (UNITED STATES)  Jan 2000,  74 (1) p173-83, ISSN
0022-538X  Journal Code: KCV
 Languages: ENGLISH
 Document type: Journal Article
 Record type: Completed
 Sleeping disease (SD) is currently a matter of concern for salmonid fish
farmers in most parts of the world. A viral etiology of SD has recently
been suspected, since virus-like particles have been observed in infected
rainbow trout cells. In salmonid-derived cell lines, the maximal rate of
virus production was observed at 10 degrees C, while little virus was
produced at 14 degrees C. Through biochemical, physicochemical, and
morphological studies, SD virus (SDV) was shown to be an enveloped virus of
roughly 60 nm in diameter. The genome consists of 12 kb of RNA, with the
appearance of a 26S subgenomic RNA during the time course of SDV
replication. The screening of a random-primed cDNA library constructed from
the genomic RNA of semipurified virions facilitated the identification of a
specific SDV cDNA clone having an open reading frame related to the
alphavirus E2 glycoproteins. To extend the comparison between SDV
structural proteins and the alphavirus protein counterparts, the nucleotide
sequence of the total 4.1-kb subgenomic RNA has been determined. The 26S
RNA encodes a 1,324-amino-acid polyprotein exhibiting typical alphavirus
structural protein organization. SDV structural proteins showed several
remarkable features compared to other alphaviruses: (i) unusually large
individual proteins, (ii) very low homology (ranging from 30 to 34%) (iii)
an unglycosylated E3 protein, and (iv) and E1 fusion domain sharing
mutations implicated in the pH threshold. Although phylogenetically related
to the Semliki Forest virus group of alphaviruses, SDV should be considered
an atypical member, able to naturally replicate in lower vertebrates.
 Record Date Created: 20000110

 9/7/6
DIALOG(R)File 155:MEDLINE(R)
10163469  99237848  PMID: 10223337
 Construction and characterization of recombinant VLPs and Semliki-Forest
virus live vectors for comparative evaluation in the SHIV monkey model.
 Notka F; Stahl-Hennig C; Dittmer U; Wolf H; Wagner R
 Institute of Medical Microbiology, University of Regensburg, Germany.
 Biological chemistry (GERMANY)  Mar 1999,  380 (3) p341-52, ISSN
1431-6730  Journal Code: CK4
 Languages: ENGLISH
 Document type: Journal Article
 Record type: Completed
 For testing of recombinant virus-like particles (VLPs) in the SHIV monkey
model, SIVmac239 Pr56gag precursor-based pseudovirions were modified by
HIV-1 gp160 derived peptides. First, well-characterized epitopes from the
HIV-1 envelope glycoprotein were inserted into the Pr56gag precursor by
replacing defined regions that were shown to be dispensable for virus
particle formation. Expression of these chimeric proteins in a baculovirus
expression system resulted in efficient assembly and release of
non-infectious, hybrid VLPs. In a second approach the HIV-1IIIB external
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glycoprotein gp120 was covalently linked to an Epstein-Barr virus derived transmembrane domain. Coexpression of the hybrid envelope derivative with the Pr56gag precursor yielded recombinant SIV derived Pr56gag particles with the HIV-1 gp120 firmly anchored on the VLP surface. Immunization of rhesus monkeys with either naked VLPs or VLPs adsorbed to alum induced substantial serum antibody titers and promoted both T helper cell and cytotoxic T lymphocyte responses. Furthermore, priming macaques with the corresponding set of recombinant Semliki-Forest viruses tended to enhance the immunological outcome. Challenge of the immunized monkeys with chimeric SHIV resulted in a clearly accelerated reduction of the plasma viremia as compared to control animals.
Record Date Created: 19990629
? t s18/7/6

18/7/6
DIALOG(R)File 155:MEDLINE(R)
05548985 88233912 PMID: 2453837
Selective recovery of foreign gene transcripts as virus-like particles in TMV-infected transgenic tobaccos.
Sleat DE; Gallie DR; Watts JW; Deom CM; Turner PC; Beachy RN; Wilson TM
Department of Virus Research, John Innes Institute, Norwich, UK.
Nucleic acids research (ENGLAND) Apr 25 1988, 16 (8) p3127-40, ISSN 0305-1048 Journal Code: O8L
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
A short origin-of-assembly sequence (OAS) located in the 30kDa movement protein gene, about 1.0kb from the 3'-end of the common strain of tobacco mosaic virus (TMV) RNA, nucleates encapsidation of the 6395-nucleotide-long genome by TMV coat protein in vitro, and presumably also in vivo. Single-stranded RNAs containing a foreign reporter gene sequence and the TMV OAS at their 5' - and 3' -ends, respectively, can be synthesized in vitro from recombinant SP6-transcription plasmids and will assemble spontaneously in vitro to form TMV-like 'pseudovirus' particles. In this paper, we show that foreign gene transcripts derived from the nuclear DNA of plants transformed by Agrobacterium tumefaciens, and which contain the TMV OAS, can be assembled into stable 'pseudovirus' particles in vivo during a systemic infection by TMV (helper). This is the first report of structural complementation between a heritable function bestowed on a transgenic plant and an infecting virus. As a route to protect, accumulate and recover a specific mRNA in vivo, in transgenic plant cells, this novel approach may find wider applications in developmental plant molecular biology.
Record Date Created: 19880630
? s flock(w)house and s3
1834 FLOCK
16637 HOUSE
52 FLOCK(W)HOUSE
2185 S3
S19 3 FLOCK(W)HOUSE AND S3
? t s19/6/1-3

19/6/1
11532403 21310087 PMID: 11414816
Specific packaging of nodaviral RNA2 requires the N-terminus of the capsid protein.
Jun 20 2001

19/6/2
10761623 20283636 PMID: 10748191
Virus maturation targets the protein capsid to concerted disassembly and unfolding.
May 26 2000

19/6/3
10051496 99096879 PMID: 9878362
Imaging RNA and dynamic protein segments with low-resolution virus crystallography: experimental design, data processing and implications of electron density maps.
Dec 18 1998
? t s19/7/1-3

19/7/1
DIALOG(R)File 155:MEDLINE(R)
11532403 21310087 PMID: 11414816
Specific packaging of nodaviral RNA2 requires the N-terminus of the capsid protein.
Marshall D; Schneemann A
Department of Molecular Biology, The Scripps Research Institute, La Jolla, California 92037, USA.
Virology (United States) Jun 20 2001, 285 (1) p165-75, ISSN 0042-6822 Journal Code: XEA
Contract/Grant No.: GM53491, GM, NIGMS
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Flock house virus (FHV), a member of the family Nodaviridae, is a nonenveloped, icosahedral insect virus whose capsids are assembled from 180 copies of a single type of coat protein. The viral genome is split between two segments of single-stranded positive-sense RNA, RNA1 and RNA2, which are packaged into a single virion. We previously demonstrated that synthesis of FHV coat protein in the baculovirus expression system results in assembly of virus-like particles whose capsids are indistinguishable from those of native virions, although the encapsidated RNA represents

primarily cellular RNA. In contrast, expression of a deletion mutant lacking N-terminal residues 2-31 results in formation of multiple types of particles which differ in size, shape, and RNA contents. We postulated that the polymorphism was imposed by the type of RNA that the coat protein selected for packaging. In the current study we tested this hypothesis by analyzing the assembly of the mutant coat protein in Drosophila cells in the presence of replicating FHV RNAs. As anticipated, the resulting particles had the same shape and dimensions as wt virions. Surprisingly, however, they contained little RNA2 while packaging of RNA1 was not affected. Small amounts of defective interfering RNAs, which emerged rapidly in the presence of the mutant coat protein, were also detected. Taken together, these observations confirm our earlier hypothesis that selection of nonviral RNAs for packaging can significantly alter the assembly process. In addition, they demonstrate that the N-terminus of the FHV coat protein contains important determinants for recognition and packaging of RNA2. Our results provide the first evidence that encapsidation of the two genomic RNAs occurs independently and that the coat protein uses different regions for the recognition of RNA1 and RNA2.

Record Date Created: 20010620

19/7/2
DIALOG(R)File 155:MEDLINE(R)
10761623 20283636 PMID: 10748191
Virus maturation targets the protein capsid to concerted disassembly and unfolding.
Oliveira AC; Gomes AM; Almeida FC; Mohana-Borges R; Valente AP; Reddy VS; Johnson JE; Silva JL
Departamento de Bioquimica Medica, Instituto de Ciencias Biomedicas, Centro Nacional de Ressonancia Magnetica Nuclear de Macromoleculas, Universidade Federal do Rio de Janeiro, 21941-590 Rio de Janeiro, RJ, Brazil.
Journal of biological chemistry (UNITED STATES) May 26 2000, 275 (21) p16037-43, ISSN 0021-9258 Journal Code: HIV
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Many animal viruses undergo post-assembly proteolytic cleavage that is required for infectivity. The role of maturation cleavage on Flock House virus was evaluated by comparing wild type (wt) and cleavage-defective mutant (D75N) Flock House virus virus-like particles. A concerted dissociation and unfolding of the mature wt particle was observed under treatment by urea, whereas the cleavage-defective mutant dissociated to folded subunits as determined by steady-state and dynamic fluorescence spectroscopy, circular dichroism, and nuclear magnetic resonance. The folded D75N alpha subunit could reassemble into capsids, whereas the yield of reassembly from unfolded cleaved wt subunits was very low. Overall, our results demonstrate that the maturation/cleavage process targets the particle for an "off pathway" disassembly, because dissociation is coupled to unfolding. The increased motions in the cleaved capsid, revealed by fluorescence and NMR, and the concerted nature of dissociation/unfolding may be crucial to make the mature particle infectious.
Record Date Created: 20000630

19/7/3
DIALOG(R)File 155:MEDLINE(R)
10051496 99096879 PMID: 9878362
Imaging RNA and dynamic protein segments with low-resolution virus crystallography: experimental design, data processing and implications of electron density maps.
Tsuruta H; Reddy VS; Wikoff WR; Johnson JE
SSRL/SLAC, Stanford University, Stanford, CA, 94309-0210, USA.
Journal of molecular biology (ENGLAND) Dec 18 1998, 284 (5) p1439-52 , ISSN 0022-2836 Journal Code: J6V
Contract/Grant No.: AI40101, AI, NIAID; GM54076, GM, NIGMS
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Single crystal diffraction data were collected from virus crystals in the resolution range of 270 to 14 A using a synchrotron X-ray source and a small-angle scattering instrument adapted for single crystal measurements. Reflections were measured from single crystals of the capsid of the double-stranded DNA bacteriophage HK97 and synthetic Flock House virus-like particles (sFHV). The quality of the low-resolution measurements was confirmed by excellent scaling statistics for both data sets. The sFHV amplitudes between 270 and 90 A resolution were closely similar to independently measured solution scattering data, and to data calculated from the Fourier transform of a uniform density sphere of 315 A diameter. A rotation function computed with the sFHV data between 70 and 20 A resolution was readily interpretable. A uniform density sphere model was used to compute phases for measured amplitudes between 270 and 68 A resolution. The calculated phases were refined and extended to 14 A resolution with real space averaging employing an external mask shape defined by the high-resolution structure. The resulting electron density map displayed regions interpretable as loosely ordered RNA that connected ordered RNA segments seen in a published 3.0 A resolution map. The published high-resolution electron density map lacked data inside 15 A resolution and the interior of the particle in that map appeared hollow. Difference electron density maps corresponding to bulk RNA were computed by subtracting the contribution of the protein shell, based on the available high-resolution atomic model, from either the cryo-electron microscopy density or the low-resolution X-ray density. Features of the RNA were closely similar in the cryo-electron microscopy and X-ray maps, demonstrating the consistency of the two imaging methods. Electron density

maps computed at 14 and 6 A resolution with the X-ray amplitudes showed that RNA contributed little to the scattering beyond 14 A resolution.

Record Date Created: 19990312
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$12.26 Estimated total session cost 3.161 DialUnits
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